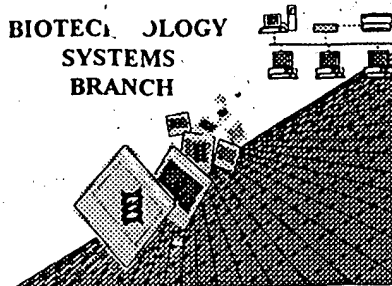# RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/828,307_

Source: _OIPE_

Date Processed by STIC: _4-23-01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

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        RAW SEQUENCE LISTING              DATE: 04/23/2001
        PATENT APPLICATION:  US/09/828,307    TIME: 13:16:47

        Input Set : A:\PTO.txt
        Output Set: N:\CRF3\04232001\I828307.raw
```

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    3 <110> APPLICANT: Mack, David
    4         Gish, Kurt
    5         Wilson, Keith
    7 <120> TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING CANCER, COMPOSITIONS, AND METHODS OF
    8         SCREENING FOR CANCER MODULATORS
   10 <130> FILE REFERENCE: A-69192-1/DJB/JJD/AMS
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/828,307
C--> 12 <141> CURRENT FILING DATE: 2001-04-06
   12 <150> PRIOR APPLICATION NUMBER: US 09/608,821
   13 <151> PRIOR FILING DATE: 2000-06-30
   15 <160> NUMBER OF SEQ ID NOS: 5
   17 <170> SOFTWARE: PatentIn version 3.0
   19 <210> SEQ ID NO: 1
   20 <211> LENGTH: 3794
   21 <212> TYPE: DNA
   22 <213> ORGANISM: Homo sapiens
   24 <220> FEATURE:
   25 <221> NAME/KEY: CDS
   26 <222> LOCATION: (38)..(2635)
   28 <400> SEQUENCE: 1
   29 ccaagttcta cctcatgttt ggaggatctt gctagct atg gcc ctc gta ctc ggc      55
   30                                         Met Ala Leu Val Leu Gly
   31                                         1               5
   33 tcc ctg ttg ctg ctg ggg ctg tgc ggg aac tcc ttt tca gga ggg cag      103
   34 Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln
   35              10              15                  20
   37 cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca      151
   38 Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala
   39          25              30                  35
   41 aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att      199
   42 Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile
   43          40              45                  50
   45 ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat      247
   46 Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp
   47 55              60              65                  70
   49 ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc      295
   50 Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser
   51              75              80                  85
   53 aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att      343
   54 Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile
   55              90              95                  100
   57 gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg      391
   58 Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu
   59              105             110                 115
   61 ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt      439
   62 Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg
   63     120             125                 130
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See p.6

RAW SEQUENCE LISTING   DATE: 04/23/2001
PATENT APPLICATION: US/09/828,307   TIME: 13:16:47

Input Set : A:\PTO.txt
Output Set: N:\CRF3\04232001\I828307.raw

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65  tgc tgt aac aaa tgt ggt gga gaa atg cac cag cga cag aag gaa aat      487
66  Cys Cys Asn Lys Cys Gly Gly Glu Met His Gln Arg Gln Lys Glu Asn
67  135              140                 145                 150
69  ggg ccc ttc ctg agg aaa tgc ttt gca atc tcc ctg ttg gtg att tgt      535
70  Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile Ser Leu Leu Val Ile Cys
71              155                 160                 165
73  ata ata ata agc att ggc atc ttc tat ggt ttt gtg gca aat cac cag      583
74  Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly Phe Val Ala Asn His Gln
75              170                 175                 180
77  gta aga acc cgg atc aaa agg agt cgg aaa ctg gca gat agc aat ttc      631
78  Val Arg Thr Arg Ile Lys Arg Ser Arg Lys Leu Ala Asp Ser Asn Phe
79          185                 190                 195
81  aag gac ttg cga act ctc ttg aat gaa act cca gag caa atc aaa tat      679
82  Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr Pro Glu Gln Ile Lys Tyr
83      200                 205                 210
85  ata ttg gcc cag tac aac act acc aag gac aag gcg ttc aca gat ctg      727
86  Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp Lys Ala Phe Thr Asp Leu
87  215                 220                 225                 230
89  aac agt atc aat tca gtg cta gga ggc gga att ctt gac cga ctg aga      775
90  Asn Ser Ile Asn Ser Val Leu Gly Gly Gly Ile Leu Asp Arg Leu Arg
91              235                 240                 245
93  ccc aac atc atc cct gtt ctt gat gag att aag tcc atg gca aca gcg      823
94  Pro Asn Ile Ile Pro Val Leu Asp Glu Ile Lys Ser Met Ala Thr Ala
95              250                 255                 260
97  atc aag gag acc aaa gag gcg ttg gag aac atg aac agc acc ttg aag      871
98  Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn Met Asn Ser Thr Leu Lys
99          265                 270                 275
101 agc ttg cac caa caa agt aca cag ctt agc agc agt ctg acc agc gtg      919
102 Ser Leu His Gln Gln Ser Thr Gln Leu Ser Ser Ser Leu Thr Ser Val
103     280                 285                 290
105 aaa act agc ctg cgg tca tct ctc aat gac cct ctg tgc ttg gtg cat      967
106 Lys Thr Ser Leu Arg Ser Ser Leu Asn Asp Pro Leu Cys Leu Val His
107 295                 300                 305                 310
109 cca tca agt gaa acc tgc aac agc atc aga ttg tct cta agc cag ctg     1015
110 Pro Ser Ser Glu Thr Cys Asn Ser Ile Arg Leu Ser Leu Ser Gln Leu
111             315                 320                 325
113 aat agc aac cct gaa ctg agg cag ctt cca ccc gtg gat gca gaa ctt     1063
114 Asn Ser Asn Pro Glu Leu Arg Gln Leu Pro Pro Val Asp Ala Glu Leu
115             330                 335                 340
117 gac aac gtt aat aac gtt ctt agg aca gat ttg gat ggc ctg gtc caa     1111
118 Asp Asn Val Asn Asn Val Leu Arg Thr Asp Leu Asp Gly Leu Val Gln
119             345                 350                 355
121 cag ggc tat caa tcc ctt aat gat ata cct gac aga gta caa cgc caa     1159
122 Gln Gly Tyr Gln Ser Leu Asn Asp Ile Pro Asp Arg Val Gln Arg Gln
123     360                 365                 370
125 acc acg act gtc gta gca ggt atc aaa agg gtc ttg aat tcc att ggt     1207
126 Thr Thr Thr Val Val Ala Gly Ile Lys Arg Val Leu Asn Ser Ile Gly
127 375                 380                 385                 390
129 tca gat atc gac aat gta act cag cgt ctt cct att cag gat ata ctc     1255
```

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130 Ser Asp Ile Asp Asn Val Thr Gln Arg Leu Pro Ile Gln Asp Ile Leu
131               395                 400                 405
133 tca gca ttc tct gtt tat gtt aat aac act gaa agt tac atc cac aga      1303
134 Ser Ala Phe Ser Val Tyr Val Asn Asn Thr Glu Ser Tyr Ile His Arg
135             410                 415                 420
137 aat tta cct aca ttg gaa gag tat gat tca tac tgg tgg ctg ggt ggc      1351
138 Asn Leu Pro Thr Leu Glu Glu Tyr Asp Ser Tyr Trp Trp Leu Gly Gly
139             425                 430                 435
141 ctg gtc atc tgc tct ctg ctg acc ctc atc gtg att ttt tac tac ctg      1399
142 Leu Val Ile Cys Ser Leu Leu Thr Leu Ile Val Ile Phe Tyr Tyr Leu
143     440                 445                 450
145 ggc tta ctg tgt ggc gtg tgc ggc tat gac agg cat gcc acc ccg acc      1447
146 Gly Leu Leu Cys Gly Val Cys Gly Tyr Asp Arg His Ala Thr Pro Thr
147 455                 460                 465                 470
149 acc cga ggc tgt gtc tcc aac acc gga ggc gtc ttc ctc atg gtt gga      1495
150 Thr Arg Gly Cys Val Ser Asn Thr Gly Gly Val Phe Leu Met Val Gly
151                 475                 480                 485
153 gtt gga tta agt ttc ctc ttt tgc tgg ata ttg atg atc att gtg gtt      1543
154 Val Gly Leu Ser Phe Leu Phe Cys Trp Ile Leu Met Ile Ile Val Val
155             490                 495                 500
157 ctt acc ttt gtc ttt ggt gca aat gtg gaa aaa ctg atc tgt gaa cct      1591
158 Leu Thr Phe Val Phe Gly Ala Asn Val Glu Lys Leu Ile Cys Glu Pro
159         505                 510                 515
161 tac acg agc aag gaa tta ttc cgg gtt ttg gat aca ccc tac tta cta      1639
162 Tyr Thr Ser Lys Glu Leu Phe Arg Val Leu Asp Thr Pro Tyr Leu Leu
163     520                 525                 530
165 aat gaa gac tgg gaa tac tat ctc tct ggg aag cta ttt aat aaa tca      1687
166 Asn Glu Asp Trp Glu Tyr Tyr Leu Ser Gly Lys Leu Phe Asn Lys Ser
167 535                 540                 545                 550
169 aaa atg aag ctc act ttt gaa caa gtt tac agt gac tgc aaa aaa aat      1735
170 Lys Met Lys Leu Thr Phe Glu Gln Val Tyr Ser Asp Cys Lys Lys Asn
171                 555                 560                 565
173 aga ggc act tac ggc act ctt cac ctg cag aac agc ttc aat atc agt      1783
174 Arg Gly Thr Tyr Gly Thr Leu His Leu Gln Asn Ser Phe Asn Ile Ser
175             570                 575                 580
177 gaa cat ctc aac att aat gag cat act gga agc ata agc agt gaa ttg      1831
178 Glu His Leu Asn Ile Asn Glu His Thr Gly Ser Ile Ser Ser Glu Leu
179         585                 590                 595
181 gaa agt ctg aag gta aat ctt aat atc ttt ctg ttg ggt gca gca gga      1879
182 Glu Ser Leu Lys Val Asn Leu Asn Ile Phe Leu Leu Gly Ala Ala Gly
183     600                 605                 610
185 aga aaa aac ctt cag gat ttt gct gct tgt gga ata gac aga atg aat      1927
186 Arg Lys Asn Leu Gln Asp Phe Ala Ala Cys Gly Ile Asp Arg Met Asn
187 615                 620                 625                 630
189 tat gac agc tac ttg gct cag act ggt aaa tcc ccc gca gga gtg aat      1975
190 Tyr Asp Ser Tyr Leu Ala Gln Thr Gly Lys Ser Pro Ala Gly Val Asn
191             635                 640                 645
193 ctt tta tca ttt gca tat gat cta gaa gca aaa gca aac agt ttg ccc      2023
194 Leu Leu Ser Phe Ala Tyr Asp Leu Glu Ala Lys Ala Asn Ser Leu Pro
```

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195            650             655             660
197 cca gga aat ttg agg aac tcc ctg aaa aga gat gca caa act att aaa    2071
198 Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys
199         665             670             675
201 aca att cac cag caa cga gtc ctt cct ata gaa caa tca ctg agc act    2119
202 Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr
203     680             685             690
205 cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg    2167
206 Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu
207 695             700             705             710
209 gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc    2215
210 Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe
211             715             720             725
213 atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat    2263
214 Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr
215             730             735             740
217 ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag    2311
218 Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu
219         745.            750             755
221 ttc tct atc agt gag aaa gtg gca tcg tgc aaa cct gtg gcc acc gct    2359
222 Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala
223     760             765             770
225 cta gat act gct gtt gat gtc ttt ctg tgt agc tac att atc gac ccc    2407
226 Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro
227 775             780             785             790
229 ttg aat ttg ttt tgg ttt ggc ata gga aaa gct act gta ttt tta ctt    2455
230 Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu
231             795             800             805
233 ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg    2503
234 Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met
235             810             815             820
237 gat tcg gag gac gtg tac gat gat gtt gaa act ata ccc atg aaa aat    2551
238 Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn
239         825             830             835
241 atg gaa aat ggt aat aat ggt tat cat aaa gat cat gta tat ggt att    2599
242 Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile
243     840             845             850
245 cac aat cct gtt atg aca agc cca tca caa cat tga tagctgatgt          2645
246 His Asn Pro Val Met Thr Ser Pro Ser Gln His
247 855             860             865
249 tgaaactgct tgagcatcag gatactcaaa gtggaaagga tcacagattt ttggtagttt    2705
251 ctgggtctac aaggactttc caaatccagg agcaacgcca gtggcaacgt agtgactcag    2765
253 gcgggcacca aggcaacggc accattggtc tctgggtagt gctttaagaa tgaacacaat    2825
255 cacgttatag tccatggtcc atcactattc aaggatgact ccctcccttc ctgtctattt    2885
257 ttgttttta ctttttaca ctgagtttct atttagacac tacaacatat ggggtgtttg    2945
259 ttcccattgg atgcatttct atcaaaactc tatcaaatgt gatggctaga ttctaacata    3005
261 ttgccatgtg tggagtgtgc tgaacacaca ccagtttaca ggaaagatgt attttgtgta    3065
263 cagtaaacgg tgtatatacc ttttgttacc acagagtttt ttaaacaaat gagtattata    3125
265 ggactttctt ctaaatgagc taaataagtc accattgact tcttggtgct gttgaaaata    3185
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267 atccattttc actaaaagtg tgtgaaacct acagcatatt cttcacgcag agattttcat   3245
269 ctattatact ttatcaaaga ttggccatgt tccacttgga aatggcatgc aaaagccatc   3305
271 atagagaaac ctgcgtaact ccatctgaca aattcaaaag agagagagag atcttgagag   3365
273 agaaatgctg ttcgttcaaa agtggagttg ttttaacaga tgccaattac ggtgtacagt   3425
275 ttaacagagt tttctgttgc attaggataa acattaattg gagtgcagct aacatgagta   3485
277 tcatcagact agtatcaagt gttctaaaat gaaatatgag aagatcctgt cacaattctt   3545
279 agatctggtg tccagcatgg atgaaacctt tgagtttggt ccctaaattt gcatgaaagc   3605
281 acaaggtaaa tattcatttg cttcaggagt ttcatgttgg atctgtcatt atcaaaagtg   3665
283 atcagcaatg aagaactggt cggacaaaat ttaacgttga tgtaatggaa ttccagatgt   3725
285 aggcattccc cccaggtctt ttcatgtgca gattgcagtt ctgattcatt tgaataaaaa   3785
287 ggaacttgg                                                           3794
290 <210> SEQ ID NO: 2
291 <211> LENGTH: 865
292 <212> TYPE: PRT
293 <213> ORGANISM: Homo sapiens
295 <400> SEQUENCE: 2
297 Met Ala Leu Val Leu Gly Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn
298 1               5                   10                  15
301 Ser Phe Ser Gly Gly Gln Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp
302             20                  25                  30
305 Asn Tyr Glu Leu Pro Ala Thr Asn Tyr Glu Thr Gln Asp Ser His Lys
306         35                  40                  45
309 Ala Gly Pro Ile Gly Ile Leu Phe Glu Leu Val His Ile Phe Leu Tyr
310     50                  55                  60
313 Val Val Gln Pro Arg Asp Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu
314 65                  70                  75                  80
317 Gln Lys Ala Tyr Glu Ser Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val
318             85                  90                  95
321 Ile Leu Gly Leu Lys Ile Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys
322             100                 105                 110
325 Cys Val Leu Gly Leu Leu Phe Ile Ile Leu Met Pro Leu Val Gly Tyr
326         115                 120                 125
329 Phe Phe Cys Met Cys Arg Cys Cys Asn Lys Cys Gly Gly Glu Met His
330     130                 135                 140
333 Gln Arg Gln Lys Glu Asn Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile
334·145                 150                 155                 160
337 Ser Leu Leu Val Ile Cys Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly
338             165                 170                 175
341 Phe Val Ala Asn His Gln Val Arg Thr Arg Ile Lys Arg Ser Arg Lys
342         180                 185                 190
345 Leu Ala Asp Ser Asn Phe Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr
346         195                 200                 205
349 Pro Glu Gln Ile Lys Tyr Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp
350     210                 215                 220
353 Lys Ala Phe Thr Asp Leu Asn Ser Ile Asn Ser Val Leu Gly Gly Gly
354 225                 230                 235                 240
357 Ile Leu Asp Arg Leu Arg Pro Asn Ile Ile Pro Val Leu Asp Glu Ile
358             245                 250                 255
361 Lys Ser Met Ala Thr Ala Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn
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<210>  5   Seg #5
<211>  5
<212>  PRT
<213>  (Artificial) ──>
<220>
<223>  Extracellular cytokine receptor motif found in many species.

<220>
<221>  UNSURE
<222>  (3)..(3)
<223>  "Xaa" at position 3 can be any amino acid.


<400>  5

Trp Ser Xaa Trp Ser
1               5
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Incomplete response for <213> as per new sequence rules section 1.823(b) See #11 on the Error Summary Sheet.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/828,307

DATE: 04/23/2001
TIME: 13:16:48

Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\04232001\I828307.raw**

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1012 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5